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RAW SEQUENCE LISTING

DATE: 01/23/2002

PATENT APPLICATION: US/09/810,501

TIME: 14:34:09

Input Set : N:\Crf3\RULE60\09810501.raw

Output Set: N:\CRF3\01232002\I810501.raw

SEQUENCE LISTING

ENTERED

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3 (1) GENERAL INFORMATION:
5     (i) APPLICANT: PAUL, PREM S.
6             MENG, XIANG-JIN
7             HALBUR, PATRICK G.
8             MOROZOV, IGOR
9             LUM, MELISSA A.
11    (ii) TITLE OF INVENTION: A POLYNUCLEIC ACID ISOLATED FROM A
12                                PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS
(PRRSV),
13                                A PROTEIN ENCODED BY THE POLYNUCLEIC ACID, A VACCINE
14                                PREPARED FROM OR CONTAINING THE POLYNUCLEIC ACID OR
W--> 15                                PROTEIN,
17    (iii) NUMBER OF SEQUENCES: 77
19    (iv) CORRESPONDENCE ADDRESS:
20            (A) ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
21                    P.C.
22            (B) STREET: 1755 S. Jefferson Davis Highway, Suite 400
23            (C) CITY: Arlington
24            (D) STATE: Virginia
25            (E) COUNTRY: U.S.A.
26            (F) ZIP: 22202
28    (v) COMPUTER READABLE FORM:
29            (A) MEDIUM TYPE: Floppy disk
30            (B) COMPUTER: IBM PC compatible
31            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
32            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
34    (vi) CURRENT APPLICATION DATA:
C--> 35            (A) APPLICATION NUMBER: US/09/810,501
C--> 36            (B) FILING DATE: 12-Mar-2001
37            (C) CLASSIFICATION:
39    (vii) PRIOR APPLICATION DATA:
40            (A) APPLICATION NUMBER: 08/301,435
41            (B) FILING DATE:
43            (A) APPLICATION NUMBER: 08/131,625
44            (B) FILING DATE: 05-OCT-1993
46    (viii) ATTORNEY/AGENT INFORMATION:
47            (A) NAME: Lavalleye, Jean-Paul M.P.
48            (B) REGISTRATION NUMBER: 31,451
49            (C) REFERENCE/DOCKET NUMBER: 4625-021-55X CIP
51    (ix) TELECOMMUNICATION INFORMATION:
52            (A) TELEPHONE: (703) 413-3000
53            (B) TELEFAX: (703) 413-2220
54            (C) TELEX: 248855 OPAT UR

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57 (2) INFORMATION FOR SEQ ID NO: 1:
59   (i) SEQUENCE CHARACTERISTICS:
60       (A) LENGTH: 22 base pairs
61       (B) TYPE: nucleic acid
62       (C) STRANDEDNESS: unknown
63       (D) TOPOLOGY: linear
65   (ii) MOLECULE TYPE: DNA (genomic)
69   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71 CGGCCGTGTG GTTCTCGCCA AT                                     22
73 (2) INFORMATION FOR SEQ ID NO: 2:
75   (i) SEQUENCE CHARACTERISTICS:
76       (A) LENGTH: 22 base pairs
77       (B) TYPE: nucleic acid
78       (C) STRANDEDNESS: unknown
79       (D) TOPOLOGY: linear
81   (ii) MOLECULE TYPE: DNA (genomic)
85   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
87 CCCATTTC CTCTAGCGAC TG                                     22
89 (2) INFORMATION FOR SEQ ID NO: 3:
91   (i) SEQUENCE CHARACTERISTICS:
92       (A) LENGTH: 20 base pairs
93       (B) TYPE: nucleic acid
94       (C) STRANDEDNESS: unknown
95       (D) TOPOLOGY: linear
97   (ii) MOLECULE TYPE: DNA (genomic)
101  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
103 GCCGCGGAAC CATCAAGCAC                                     20
105 (2) INFORMATION FOR SEQ ID NO: 4:
107   (i) SEQUENCE CHARACTERISTICS:
108       (A) LENGTH: 20 base pairs
109       (B) TYPE: nucleic acid
110       (C) STRANDEDNESS: unknown
111       (D) TOPOLOGY: linear
113   (ii) MOLECULE TYPE: DNA (genomic)
117   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
119 CAACTTGACG CTATGTGAGC                                     20
121 (2) INFORMATION FOR SEQ ID NO: 5:
123   (i) SEQUENCE CHARACTERISTICS:
124       (A) LENGTH: 20 base pairs
125       (B) TYPE: nucleic acid
126       (C) STRANDEDNESS: unknown
127       (D) TOPOLOGY: linear
129   (ii) MOLECULE TYPE: DNA (genomic)
133   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
135 GCGGTCTGGA TTGACGACAG                                     20
137 (2) INFORMATION FOR SEQ ID NO: 6:
139   (i) SEQUENCE CHARACTERISTICS:
140       (A) LENGTH: 20 base pairs
141       (B) TYPE: nucleic acid

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142         (C) STRANDEDNESS: unknown
143         (D) TOPOLOGY: linear
145     (ii) MOLECULE TYPE: DNA (genomic)
149     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
151 GACTGCTAGG GCTTCTGCAC                                     20
153 (2) INFORMATION FOR SEQ ID NO: 7:
155     (i) SEQUENCE CHARACTERISTICS:
156         (A) LENGTH: 20 base pairs
157         (B) TYPE: nucleic acid
158         (C) STRANDEDNESS: unknown
159         (D) TOPOLOGY: linear
161     (ii) MOLECULE TYPE: DNA (genomic)
165     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
167 GCCATTCAGC TCACATAGCG                                     20
169 (2) INFORMATION FOR SEQ ID NO: 8:
171     (i) SEQUENCE CHARACTERISTICS:
172         (A) LENGTH: 19 base pairs
173         (B) TYPE: nucleic acid
174         (C) STRANDEDNESS: unknown
175         (D) TOPOLOGY: linear
177     (ii) MOLECULE TYPE: DNA (genomic)
181     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
183 CTCGTCAAGT ATGCCCGGT                                     19
185 (2) INFORMATION FOR SEQ ID NO: 9:
187     (i) SEQUENCE CHARACTERISTICS:
188         (A) LENGTH: 19 base pairs
189         (B) TYPE: nucleic acid
190         (C) STRANDEDNESS: unknown
191         (D) TOPOLOGY: linear
193     (ii) MOLECULE TYPE: DNA (genomic)
197     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
199 GCCATTCGCC TGACTGTCA                                     19
201 (2) INFORMATION FOR SEQ ID NO: 10:
203     (i) SEQUENCE CHARACTERISTICS:
204         (A) LENGTH: 19 base pairs
205         (B) TYPE: nucleic acid
206         (C) STRANDEDNESS: unknown
207         (D) TOPOLOGY: linear
209     (ii) MOLECULE TYPE: DNA (genomic)
213     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
215 TTGACGAGGA CTTCGGCTG                                     19
217 (2) INFORMATION FOR SEQ ID NO: 11:
219     (i) SEQUENCE CHARACTERISTICS:
220         (A) LENGTH: 20 base pairs
221         (B) TYPE: nucleic acid
222         (C) STRANDEDNESS: unknown
223         (D) TOPOLOGY: linear
225     (ii) MOLECULE TYPE: DNA (genomic)
229     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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231 GCTCTACCTG CAATTCTGTG                                     20
233 (2) INFORMATION FOR SEQ ID NO: 12:
235     (i) SEQUENCE CHARACTERISTICS:
236         (A) LENGTH: 20 base pairs
237         (B) TYPE: nucleic acid
238         (C) STRANDEDNESS: unknown
239         (D) TOPOLOGY: linear
241     (ii) MOLECULE TYPE: DNA (genomic)
245     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
247 GTGTATAGGA CCGGCAACCG                                     20
249 (2) INFORMATION FOR SEQ ID NO: 13:
251     (i) SEQUENCE CHARACTERISTICS:
252         (A) LENGTH: 2062 base pairs
253         (B) TYPE: nucleic acid
254         (C) STRANDEDNESS: unknown
255         (D) TOPOLOGY: unknown
257     (ii) MOLECULE TYPE: cDNA
259     (vi) ORIGINAL SOURCE:
260         (A) ORGANISM: porcine reproductive and respiratory syndrome
261                        virus
262         (B) STRAIN: Iowa
263         (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)
266     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
268 GGCAGGCTTT GCTGTCTCTCC AAGACATCAG TTGCCTTAGG CATCGCAACT CGGCCTCTGA      60
270 GGCGATTTCG AAAGTCCCTC AGTGCCGCAC GGCGATAGGG ACACCCGTGT ATATCACTGT      120
272 CACAGCCAAT GTTACCGATG AGAATTATTT GCATTCTCTT GATCTTCTCA TGCTTTCTTC      180
274 TTGCCTTTTC TATGCTTCTG AGATGAGTGA AAAGGGATTT AAGGTGGTAT TTGGCAATGT      240
276 GTCAGGCATC GTGGCAGTGT GCGTCAACTT CACCAGTTAC GTCCAACATG TCAAGGAATT      300
278 TACCCAACGT TCCTTGGTAG TTGACCATGT GCGGCTGCTC CATTTTCATGA CGCCCAGAGAC      360
280 CATGAGGTGG GCAACTGTTT TAGCCTGTCT TTTTGGCATT CTGTTGGCAA TTTGAATGTT      420
282 TAAGTATGTT GGGGAAATGC TTGACCGCGG GCTGTTGCTC GCAATTGCTT TTTTGTGGGT      480
284 GTATCGTGCC GTCTTGTTTT GTTGCGCTCG TCAGCGCCAA CGGGAACAGC GGCTCAAATT      540
286 TACAGCTGAT TTACAACCTG ACGCTATGTG AGCTGAATGG CACAGATTGG CTAGCTAATA      600
288 AATTTGACTG GGCAGTGAGG TGTTTTGTCA TTTTTCCTGT GTTGAATCAC ATTGTCTCTT      660
290 ATGGTGCCCT CACTACTAGC CATTTCTTGG ACACAGTCGG TCTGGTCACT GTGTCTACCG      720
292 CTGGGTTTGT TCACGGGCGG TATGTTCTGA GTAGCATGTA CGCGGTCTGT GCCCTGGCTG      780
294 CGTTGATTTG CTTTCGTCATT AGGCTTGCGA AGAATTGCAT GTCCTGGCGC TACTCATGTA      840
296 CCAGATATAC CAACTTTCTT CTGGACACTA AGGGCAGACT CTATCGTTGG CGGTCGCCTG      900
298 TCATCATAGA GAAAAGGGGC AAAGTTGAGG TCGAAGGTCA CCTGATCGAC CTCAAAAGAG      960
300 TTGTGCTTGA TGGTTCCGCG GCTACCCCTG TAACCAGAGT TTCAGCGGAA CAATGGAGTC     1020
302 TGCTTTAGAT GACTTCTGTC ATGATAGCAC GGCTCCACAA AAGGTGCTCT TGGCGTTTTT      1080
304 TATTACCTAC ACGCCAGTGA TGATATATGC CCTAAAGGTG AGTCGCGGCC GACTGCTAGG      1140
306 GCTTCTGCAC CTTTGTGCTT TCCTGAATTG TGCTTTCACC TTCGGGTACA TGACATTCGT      1200
308 GCACTTTCAG AGTACAAATA AGGTCGCGCT CACTATGGGA GCAGTAGTTG CACTCCTTTG      1260
310 GGGGGTGTAC TCAGCCATAG AAACCTGGAA ATTCATCACC TCCAGATGCC GTTTGTGCTT      1320
312 GCTAGGCCGC AAGTACATTC TGGCCCCTGC CCACCACGTT GAAAGTGCCG CAGGCTTTCA      1380
314 TCCGATTGCG GCAAATGATA ACCACGCATT TGTCGTCCGG CGTCCCGGCT CCACTACGGT      1440
316 CAACGGCACA TTGGTGCCCG GGTAAAAAAG CCTCGTGTTG GGTGGCAGAA AAGCTGTTAA      1500
318 ACAGGGAGTG GTAAACCTTG TTAAATATGC CAAATAACAC CGGCAAGCAG CAGAAGAGAA      1560

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320 AGAAGGGGGA TGGCCAGCCA GTCAATCAGC TGTGCCAGAT GCTGGGTAAG ATCATCGCTC      1620
322 ACCAAAACCA GTCCAGAGGC AAGGGACCGG GAAAGAAAAA TAAGAAGAAA AACCCGGAGA      1680
324 AGCCCCATTT CCCTCTAGCG ACTGAAGATG ATGTCAGACA TCACTTTACC CCTAGTGAGC      1740
326 GTCAATTGTG TCTGTCTGCA ATCCAGACCG CCTTTAATCA AGGCGCTGGG ACTTGACCC      1800
328 TGTCAGATTC AGGGAGGATA AGTTACACTG TGGAGTTTAG TTTGCCTACG CATCATACTG      1860
330 TGCGCCTGAT CCGCGTCACA GCATCACCT CAGCATGATG GGCTGGCATT CTTGAGGCAT      1920
332 CCCAGTGTTC GAATTGGAAG AATGCGTGGT GAATGGCACT GATTGACATT GTGCCTCTAA      1980
334 GTCACCTATT CAATTAGGGC GACCGTGTGG GGGTAAGATT TAATTGGCGA GAACCACACG      2040
336 GCCGAAATTA AAAAAAAAAA AA                                     2062
338 (2) INFORMATION FOR SEQ ID NO: 14:
340     (i) SEQUENCE CHARACTERISTICS:
341         (A) LENGTH: 603 base pairs
342         (B) TYPE: nucleic acid
343         (C) STRANDEDNESS: unknown
344         (D) TOPOLOGY: unknown
346     (ii) MOLECULE TYPE: cDNA
348     (vi) ORIGINAL SOURCE:
349         (A) ORGANISM: porcine reproductive and respiratory syndrome
350                     virus
351         (B) STRAIN: Iowa
352         (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)
354     (ix) FEATURE:
355         (A) NAME/KEY: CDS
356         (B) LOCATION: 1..600
359     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
361 ATG TTG GGG AAA TGC TTG ACC GCG GGC TGT TGC TCG CAA TTG CTT TTT      48
362 Met Leu Gly Lys Cys Leu Thr Ala Gly Cys Cys Ser Gln Leu Leu Phe
363   1           5           10           15
365 TTG TGG TGT ATC GTG CCG TCT TGT TTT GTT GCG CTC GTC AGC GCC AAC      96
366 Leu Trp Cys Ile Val Pro Ser Cys Phe Val Ala Leu Val Ser Ala Asn
367           20           25           30
369 GGG AAC AGC GGC TCA AAT TTA CAG CTG ATT TAC AAC TTG ACG CTA TGT      144
370 Gly Asn Ser Gly Ser Asn Leu Gln Leu Ile Tyr Asn Leu Thr Leu Cys
371           35           40           45
373 GAG CTG AAT GGC ACA GAT TGG CTA GCT AAT AAA TTT GAC TGG GCA GTG      192
374 Glu Leu Asn Gly Thr Asp Trp Leu Ala Asn Lys Phe Asp Trp Ala Val
375           50           55           60
377 GAG TGT TTT GTC ATT TTT CCT GTG TTG ACT CAC ATT GTC TCT TAT GGT      240
378 Glu Cys Phe Val Ile Phe Pro Val Leu Thr His Ile Val Ser Tyr Gly
379   65           70           75           80
381 GCC CTC ACT ACT AGC CAT TTC CTT GAC ACA GTC GGT CTG GTC ACT GTG      288
382 Ala Leu Thr Thr Ser His Phe Leu Asp Thr Val Gly Leu Val Thr Val
383           85           90           95
385 TCT ACC GCT GGG TTT GTT CAC GGG CGG TAT GTT CTG AGT AGC ATG TAC      336
386 Ser Thr Ala Gly Phe Val His Gly Arg Tyr Val Leu Ser Ser Met Tyr
387           100          105          110
389 GCG GTC TGT GCC CTG GCT GCG TTG ATT TGC TTC GTC ATT AGG CTT GCG      384
390 Ala Val Cys Ala Leu Ala Ala Leu Ile Cys Phe Val Ile Arg Leu Ala
391           115          120          125

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\01232002\I810501.raw

L:35 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:15 M:259 W: Allowed number of lines exceeded, (ii) TITLE OF INVENTION: